

SEQUENCE LISTING

<110> Presnell, Scott R.
 Xu, Wenfeng
 Kindsvogel, Wayne
 Chen, Zhi

<120> Human Cytokine Receptor

<130> 99-93

<150> US 60/169,049

<151> 1999-12-03

<150> US 60/232,219

<151> 2000-09-13

<150> US 60/244,610

<151> 2000-10-31

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<211> 2149

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(693)

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1				5					10					15		

act	ggt	gta	gca	gga	act	cag	tca	acg	cat	gag	tct	ctg	aag	cct	cag	96
Thr	Gly	Val	Ala	Gly	Thr	Gln	Ser	Thr	His	Glu	Ser	Leu	Lys	Pro	Gln	
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00728911-120100

agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag	144
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln	
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cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac	192
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr	
50 55 60	
aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt	240
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly	
65 70 75 80	
act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag	288
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln	
85 90 95	
gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca	336
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser	
100 105 110	
gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata	384
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile	
115 120 125	
gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta	432
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val	
130 135 140	
att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat	480
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn	
145 150 155 160	
gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att	528
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile	
165 170 175	
aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga	576
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg	
180 185 190	
gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg	624
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val	
195 200 205	

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gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga agt gaa 672
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220

gag aga tgt gtg gaa att cca tgacttggtg aatttggtat tcagcaatgt 723
 Glu Arg Cys Val Glu Ile Pro
 225 230

ggaaattcta aagctccctg agaacaggat gactcgtggt tgaaggatct tatttaaaat 783
 tgtttttgta ttttcttaaa gcaatattca ctgttacacc ttggggactt ctttgtttat 843
 ccattctttt atcctttata tttcatttta aactatatatt gaacgacatt cccccgaaa 903
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 taaaaaatat tcagaaatgt attggggggt ggaggagaat aagaggcaga gcaagagcta 2043
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<211> 231

<212> PRT

<213> Homo sapiens

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Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 20 25 30
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 35 40 45
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60
 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95
 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125
 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140
 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160
 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175
 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190
 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220
 Glu Arg Cys Val Glu Ile Pro
 225 230

<210> 3

<211> 693

<212> DNA

<213> Artificial Sequence

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<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:2.

<221> misc_feature

<222> (1)...(693)

<223> n = A,T,C or G

<400> 3

09728911.120100

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<210> 4
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<213> Artificial Sequence
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<400> 4

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<210> 5
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acccttgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	180
aactggtacg	tggacggcgt	ggagggtgat	aatgccaaga	caaagccgcg	ggaggagcag	240
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	300
ggcaaggagt	acaagtgcaa	ggtctccaac	aaagccctcc	catectccat	cgagaaaacc	360
atctccaaag	ccaaagggca	gccccgagaa	ccacagggtgt	acaccctgcc	cccatcccgg	420
gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatcccagc	480
gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	540
cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	600
aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	660
tacacqcaqa	agagcctctc	cctgtctccg	ggtaaataa			699

<210> 6
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<210> 7
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 <223> Oligonucleotide primer ZC29182

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gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc gag ttg aga cgc 96
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
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ttc cgt aga tcc 108

Phe Arg Arg Ser
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<210> 9
<211> 36
<212> PRT
<213> Homo sapiens

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Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
20 25 30

Phe Arg Arg Ser
35

<210> 10
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<223> Glu-Glu (CEE) Tag amino acid sequence

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<213> Artificial Sequence

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<223> His Tag amino acid sequence

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His His His His His His
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<210> 13

<211> 210

<212> PRT

<213> Homo sapiens

<400> 13

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Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr Lys Ile Tyr Gly Gln
35 40 45
Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly Thr Gln Glu Leu Ser
50 55 60
Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln Glu Pro Tyr Tyr Gly
65 70 75 80
Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser Glu Trp Ser Met Thr
85 90 95
Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile Asp Pro Pro Val Met
100 105 110
Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val Ile Leu His Ala Pro
115 120 125
Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn Val Ser Ile Glu Asp
130 135 140
Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile Asn Asn Ser Leu Glu
145 150 155 160
Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg Ala Val Glu Ile Glu
165 170 175
Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val Ala Glu Ile Tyr Gln
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Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu Glu Arg Cys Val Glu
195 200 205
Ile Pro
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Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu	
15 20 25	
gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac	149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp	
30 35 40	
aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg	197
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu	
45 50 55	
gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att	245
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile	
60 65 70 75	
ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg	293
Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu	
80 85 90	
atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa	341
Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln	
95 100 105	
tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc	389
Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala	
110 115 120	

001021-120100

agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg 437
 Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu
 125 130 135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485
 His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu
 140 145 150 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533
 Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Phe
 160 165 170

atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac 587
 Met Ser Leu Arg Asn Ala Cys Ile
 175

taacccccctt tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca 647
 aaaggaagat gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt 707
 tagttacaaa ggaaaccaat gccacttttg tttataagac cagaaggtag actttctaag 767
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 aaaccctaa atagcttcat gtttccataa tcagtacttt atatttataa atgtatttat 947
 tattattata agactgcatt ttatttataat cattttatta atatggattt atttatagaa 1007
 acatcattcg atattgctac ttgagtgtaa ggctaataat gatatttatg acaataatta 1067
 tagagctata acatgtttat ttgacctcaa taaacacttg gatatccta 1116

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<211> 179

<212> PRT

<213> Homo sapiens

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 20 25 30
 Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
 35 40 45
 Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 50 55 60
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 65 70 75 80

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His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
 85 90 95
 Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
 100 105 110
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
 115 120 125
 Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
 130 135 140
 Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
 145 150 155 160
 Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
 165 170 175
 Ala Cys Ile

<210> 16

<211> 23

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<223> Oligonucleotide primer ZC25963

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23

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<223> Oligonucleotide primer ZC28354

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accaacaaag agccattgac ttg

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001021" TT682460

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<212> DNA
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<210> 21
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<223> Oligonucleotide primer ZC17600

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<400> 23
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<222> (34)...(1755)

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1 5

ttg act gtg gga tcc ctg gct gct cac gcc cct gag gac ccc tcg gat 102
Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp
10 15 20

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg 150
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu
25 30 35

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc 198
Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile
40 45 50 55

gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt 246

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Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys	
60 65 70	
cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac	294
Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn	
75 80 85	
ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc	342
Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly	
90 95 100	
cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act	390
Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr	
105 110 115	
acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att	438
Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile	
120 125 130 135	
cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc	486
Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly	
140 145 150	
cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta	534
His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu	
155 160 165	
gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag	582
Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln	
170 175 180	
aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc	630
Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly	
185 190 195	
acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac	678
Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr	
200 205 210 215	
atg tgc cga gtg aag aca ctg cca gac cgg aca tgg acc tac tcc ttc	726
Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe	
220 225 230	

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Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys	
235 240 245	
tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc	822
Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser	
250 255 260	
ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag	870
Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln	
265 270 275	
gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg	918
Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu	
280 285 290 295	
gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag	966
Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu	
300 305 310	
ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta	1014
Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu	
315 320 325	
ggg cag cca gac atc tcc atc ctc cag ccc tcc aac gtg cca cct ccc	1062
Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro	
330 335 340	
cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc	1110
Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val	
345 350 355	
ggg ccc cca tcc tat gca cct cag gtg acc ccc gaa gct caa ttc cca	1158
Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro	
360 365 370 375	
ttc tac gcc cca cag gcc atc tct aag gtc cag cct tcc tcc tat gcc	1206
Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala	
380 385 390	
cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg	1254
Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met	
395 400 405	

001021 1682260

gaa ggt tct ggc aaa gac tcc ccc act ggg aca ctt tct agt cct aaa 1302
 Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys
 410 415 420

cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc 1350
 His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser
 425 430 435

tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg 1398
 Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met
 440 445 450 455

gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc 1446
 Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys
 460 465 470

aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg 1494
 Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly
 475 480 485

aca cca cag tac cta aag ggc cag ctc ccc ctc ctc tcc tca gtc cag 1542
 Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln
 490 495 500

atc gag ggc cac ccc atg tcc ctc cct ttg caa cct cct tcc ggt cca 1590
 Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro
 505 510 515

tgt tcc ccc tcg gac caa ggt cca agt ccc tgg ggc ctg ctg gag tcc 1638
 Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser
 520 525 530 535

ctt gtg tgt ccc aag gat gaa gcc aag agc cca gcc cct gag acc tca 1686
 Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser
 540 545 550

gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc 1734
 Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala
 555 560 565

ctg act gtg cag tgg gag tcc tgaggggaat gggaaaggct tggtgcttcc 1785

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Leu Thr Val Gln Trp Glu Ser
570

tccctgtccc	taccagtggt	cacatccttg	gctgtcaatc	ccatgcctgc	ccatgccaca	1845
cactctgcga	tctggcctca	gacgggtgcc	cttgagagaa	gcagagggag	tggcatgcag	1905
ggcccctgcc	atgggtgcgc	tcctcaccgg	aacaaagcag	catgataagg	actgcagcgg	1965
gggagctctg	gggagcagct	tgtgtagaca	agcgcgtgct	cgctgagccc	tgcaaggcag	2025
aaatgacagt	gcaaggagga	aatgcaggga	aactcccagag	gtccagagcc	ccacctccta	2085
acaccatgga	ttcaaagtgc	tcagggaatt	tgcctctcct	tgccccattc	ctggccagtt	2145
tcacaatcta	gctcgacaga	gcatgaggcc	cctgcctcct	ctgtcattgt	tcaaagggtg	2205
gaagagagcc	tggaaaagaa	ccaggcctgg	aaaagaacca	gaaggaggct	gggcagaacc	2265
agaacaacct	gcattctgc	caaggccagg	gccagcagga	cggcaggact	ctagggaggg	2325
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gctgtggccc	ctggacgggt	acaataacac	actgtactga	tgtcacaact	ttgcaagctc	2565
tgccttgggt	tcagcccata	tgggctcaaa	ttccagcctc	accactcaca	agctgtgtga	2625
cttcaaacia	atgaaatcag	tgcccagaac	ctcggtttcc	tcactctgtaa	tgtggggatc	2685
ataacaccta	cctcatggag	ttgtggtgaa	gatgaaatga	agtcatgtct	ttaaagtgtc	2745
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<211> 574

<212> PRT

<213> Homo sapiens

<400> 25

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Ala	Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser
			20					25					30		
Ser	Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr
	35					40					45				
Pro	Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp
	50					55					60				
Trp	Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn
65				70					75					80	
Leu	Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val
			85					90					95		
Thr	Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg
			100					105					110		

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Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys
		115					120					125			
Ile	Ser	Lys	Val	Arg	Ser	Ile	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr
		130					135					140			
Pro	Ile	Arg	Ala	Gly	Asp	Gly	His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe
145					150						155				160
His	Asp	Leu	Phe	Tyr	His	Leu	Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln
				165					170					175	
Met	His	Leu	Gly	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr
			180					185					190		
Pro	Asp	Thr	Glu	Phe	Leu	Gly	Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp
		195					200					205			
Ala	Lys	Glu	Ser	Ala	Pro	Tyr	Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp
		210				215					220				
Arg	Thr	Trp	Thr	Tyr	Ser	Phe	Ser	Gly	Ala	Phe	Leu	Phe	Ser	Met	Gly
225					230					235					240
Phe	Leu	Val	Ala	Val	Leu	Cys	Tyr	Leu	Ser	Tyr	Arg	Tyr	Val	Thr	Lys
				245					250					255	
Pro	Pro	Ala	Pro	Pro	Asn	Ser	Leu	Asn	Val	Gln	Arg	Val	Leu	Thr	Phe
			260					265					270		
Gln	Pro	Leu	Arg	Phe	Ile	Gln	Glu	His	Val	Leu	Ile	Pro	Val	Phe	Asp
		275					280					285			
Leu	Ser	Gly	Pro	Ser	Ser	Leu	Ala	Gln	Pro	Val	Gln	Tyr	Ser	Gln	Ile
		290				295					300				
Arg	Val	Ser	Gly	Pro	Arg	Glu	Pro	Ala	Gly	Ala	Pro	Gln	Arg	His	Ser
305					310					315					320
Leu	Ser	Glu	Ile	Thr	Tyr	Leu	Gly	Gln	Pro	Asp	Ile	Ser	Ile	Leu	Gln
				325					330					335	
Pro	Ser	Asn	Val	Pro	Pro	Pro	Gln	Ile	Leu	Ser	Pro	Leu	Ser	Tyr	Ala
			340					345					350		
Pro	Asn	Ala	Ala	Pro	Glu	Val	Gly	Pro	Pro	Ser	Tyr	Ala	Pro	Gln	Val
		355					360					365			
Thr	Pro	Glu	Ala	Gln	Phe	Pro	Phe	Tyr	Ala	Pro	Gln	Ala	Ile	Ser	Lys
						375					380				
Val	Gln	Pro	Ser	Ser	Tyr	Ala	Pro	Gln	Ala	Thr	Pro	Asp	Ser	Trp	Pro
385					390					395					400
Pro	Ser	Tyr	Gly	Val	Cys	Met	Glu	Gly	Ser	Gly	Lys	Asp	Ser	Pro	Thr
				405					410					415	
Gly	Thr	Leu	Ser	Ser	Pro	Lys	His	Leu	Arg	Pro	Lys	Gly	Gln	Leu	Gln
			420					425					430		
Lys	Glu	Pro	Pro	Ala	Gly	Ser	Cys	Met	Leu	Gly	Gly	Leu	Ser	Leu	Gln
		435					440					445			

Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
 450 455 460
 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
 465 470 475 480
 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
 485 490 495
 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
 500 505 510
 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
 515 520 525
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
 530 535 540
 Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp
 545 550 555 560
 Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser
 565 570

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<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker ZC13252

<400> 26

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39

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<213> Artificial Sequence

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27

<210> 28

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<212> DNA

<213> Artificial Sequence

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<220>

<223> Oligonucleotide primer ZC28590

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36

<210> 29

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<223> Oligonucleotide primer ZC28580

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ttgggatcca atgcaggcat ttctcagaga cat

33

<210> 30

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC25963

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23

<210> 31

<211> 23

<212> DNA

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<223> Oligonucleotide primer ZC25964

<400> 31

gttcttgagt accccaacag tct

23

<210> 32

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<212> DNA

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<223> Oligonucleotide primer ZC14666

<400> 32

agccaccaag atgactga

18

<210> 33

<211> 22

<212> DNA

<213> Artificial Sequence

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22

<210> 34

<211> 211

<212> PRT

<213> Homo sapiens

<400> 34

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Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr	Pro	20	25	30	
Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp	Trp	35	40	45	
Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	Leu	50	55	60	
Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	Thr	65	70	75	80
Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	Phe	85	90	95	
Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	100	105	110	
Ser	Lys	Val	Arg	Ser	Ile	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro	115	120	125	
Ile	Arg	Ala	Gly	Asp	Gly	His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	His	130	135	140	

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Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
 145 150 155 160
 His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
 165 170 175
 Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala
 180 185 190
 Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
 195 200 205
 Thr Trp Thr
 210

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 Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met
 35 40 45
 Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly
 50 55 60
 Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp
 65 70 75 80
 Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro
 85 90 95
 Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe
 100 105 110
 Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn
 115 120 125
 Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr
 130 135 140
 Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg
 145 150 155 160
 Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
 165 170 175
 Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln
 180 185 190
 Thr Thr His Asp Glu Thr Val
 195

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<210> 36
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 <212> PRT
 <213> Homo sapiens

<400> 36

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Glu	Ala	Glu	Phe	Phe	His	His	Ile	Leu	His	Trp	Thr	Pro	Ile	Pro	Asn
			20					25					30		
Gln	Ser	Glu	Ser	Thr	Cys	Tyr	Glu	Val	Ala	Leu	Leu	Arg	Tyr	Gly	Ile
		35					40					45			
Glu	Ser	Trp	Asn	Ser	Ile	Ser	Asn	Cys	Ser	Gln	Thr	Leu	Ser	Tyr	Asp
		50				55					60				
Leu	Thr	Ala	Val	Thr	Leu	Asp	Leu	Tyr	His	Ser	Asn	Gly	Tyr	Arg	Ala
65					70					75				80	
Arg	Val	Arg	Ala	Val	Asp	Gly	Ser	Arg	His	Ser	Asn	Trp	Thr	Val	Thr
				85					90					95	
Asn	Thr	Arg	Phe	Ser	Val	Asp	Glu	Val	Thr	Leu	Thr	Val	Gly	Ser	Val
			100					105					110		
Asn	Leu	Glu	Ile	His	Asn	Gly	Phe	Ile	Leu	Gly	Lys	Ile	Gln	Leu	Pro
		115				120						125			
Arg	Pro	Lys	Met	Ala	Pro	Ala	Asn	Asp	Thr	Tyr	Glu	Ser	Ile	Phe	Ser
		130				135					140				
His	Phe	Arg	Glu	Tyr	Glu	Ile	Ala	Ile	Arg	Lys	Val	Pro	Gly	Asn	Phe
145					150					155				160	
Thr	Phe	Thr	His	Lys	Lys	Val	Lys	His	Glu	Asn	Phe	Ser	Leu	Leu	Thr
				165					170					175	
Ser	Gly	Glu	Val	Gly	Glu	Phe	Cys	Val	Gln	Val	Lys	Pro	Ser	Val	Ala
		180						185					190		
Ser	Arg	Ser	Asn	Lys	Gly	Met	Trp	Ser	Lys	Glu	Glu	Cys	Ile	Ser	Leu
		195					200					205			
Thr	Arg	Gln													
		210													

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